

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Process for the fermentative preparation of
L-amino acids using strains of the
Enterobacteriaceae family.

10 <130> 000425 BT

<140>
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15 <160> 19

<170> PatentIn Ver. 2.1

20 <210> 1
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35 atc agt gac gta cat gat atc gtt tac aac cca agc tac gac ctg ctg 96
Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
20 25 30

40 tat cag gaa gag ctc gat ccg agc ctg aca ggt tat gag cgc ggg gtg 144
Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
35 40 45

tta act aat ctg ggt gcc gtt gcc gtc gat acc ggg atc ttc acc ggt 192
Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
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45 cgt tca cca aaa gat aag tat atc gtc cgt gac gat acc act cgc gat 240
Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
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50 act ttc tgg tgg gca gac aaa ggc aaa ggt aag aac gac aac aaa cct 288
Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
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Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
100 105 110

60 ctt tcc ggc aaa cgt ctg ttc gtt gtc gac gct ttc tgt ggt gcg aac 384
Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
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10 ccg acg cca acc ttc tcc gct tgc ttc ggc gcg gca ttc ctg tcg ctg 1248
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 405 410 415

15 cac ccg act cag tac gca gaa gtg ctg gtg aaa cgt atg cag gcg gcg 1296
 His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
 420 425 430

20 ggc gcg cag gct tat ctg gtt aac act ggc tgg aac ggc act ggc aaa 1344
 Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
 435 440 445

25 cgt atc tcg att aaa gat acc cgc gcc att atc gac gcc atc ctc aac 1392
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30 ggt tcg ctg gat aat gca gaa acc ttc act ctg ccg atg ttt aac ctg 1440
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35 gcg atc cca acc gaa ctg ccg ggc gta gac acg aag att ctc gat ccg 1488
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40 cgt aac acc tac gct tct ccg gaa cag tgg cag gaa aaa gcc gaa acc 1536
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45 ctg gcg aaa ctg ttt atc gac aac ttc gat aaa tac acc gac acc cct 1584
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 35 40 45

Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
 50 55 60
 5 Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
 65 70 75 80
 Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
 85 90 95
 10 Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
 100 105 110
 Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
 115 120 125
 15 Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
 130 135 140
 20 Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
 145 150 155 160
 Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
 165 170 175
 25 Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
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 Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
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 30 Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
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 35 Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
 225 230 235 240
 Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
 245 250 255
 40 Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
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 Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
 275 280 285
 45 Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
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 50 Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
 305 310 315 320
 Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
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 55 Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
 340 345 350
 His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
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 60

Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
370 375 380

5 Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
385 390 395 400

Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
405 410 415

10 His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
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Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
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15 Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
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Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
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<223> Technical DNA/residues of the polylinker sequence

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 aaggttatct tcttgactgc tgatgctttc ggctgtgtgc cgcggtttc tcgcctgact 720
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 <212> DNA
 35 <213> Escherichia coli

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 <222> (1)..(598)
 45 <223> 5' region of the delta pckA allele

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 <222> (599)..(618)
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 <222> (619)..(1291)
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 <222> (1292)..(1294)
 60 <223> Stop codon of the delta pckA allele

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000425 BT / AL1

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	ctgacagggt	atgagcgcgg	ggtgttaact	aatctgggtg	ccgttgccgt	cgataccggg	180
5	atcttcaccg	gtcgttcacc	aaaagataag	tatatcgccc	gtgacgatac	cactcgcgat	240
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 5 <213> Escherichia coli

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 20 <223> 3' flank of the ytfP-yjfa region

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 25 <223> ATG codon of the truncated ORF ytfP

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 30 <223> ATG codon of the truncated ORF yjfa

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 ccagattgtg ggtaaaatcg gcgagacgtt tggcgtaagc aatttagcgc tcgacaccca 180
 gggagtaggc gactcctccc aggtagtggc cagcggctat gtattgccag gtctgcaagt 240
 gaaatacggc gtgggtatat ttgactctat agcaaacactc acgttacgtt atcgctgat 300
 25 gcctaagcta tatctggaag ccgtgtcttg tgtagaccag gcaactggatt tgctctatca 360
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000425 BT / AL1